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## Salicylaldoxime-III at 150 K

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## Key indicators

Single-crystal X-ray study

$T = 150$  K

Mean  $\sigma(\text{C}-\text{C}) = 0.002$  Å

$R$  factor = 0.033

$wR$  factor = 0.079

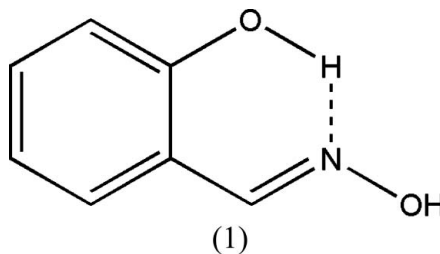
Data-to-parameter ratio = 9.7

For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

Salicylaldoxime derivatives crystallize in either hydrogen-bonded ring or chain motifs. A polymorph of the parent compound, salicylaldoxime, characterized by ring formation, has been known for some time. We now report a new polymorph of salicylaldoxime (2-hydroxybenzaldehyde oxime,  $\text{C}_7\text{H}_7\text{NO}_2$ ), which exhibits chain formation and which has two molecules per asymmetric unit.  $\pi$ - $\pi$  stacking interactions occur between the chains. We refer to this polymorph as salicylaldoxime-III.

## Comment

Salicylaldoximes bearing branched alkyl chains are used as extractants to effect the separation and concentration operations in the hydrometallurgical recovery of copper, accounting for around 30% of annual production (Kordosky, 2002). The  $\text{N}_2\text{O}_2^{2-}$  donor set in bis-salicylaldoxime complexes is stabilized by interligand hydrogen bonds, forming a pseudo-macrocylic arrangement (*e.g.* Fig. 1*a*). The high selectivity of salicylaldoximes for copper over other metal ions is the result of the compatibility of the size of the cavity at the centre of the pseudo-macrocycle and the ionic radius of  $\text{Cu}^{2+}$  (Smith *et al.*, 2002).

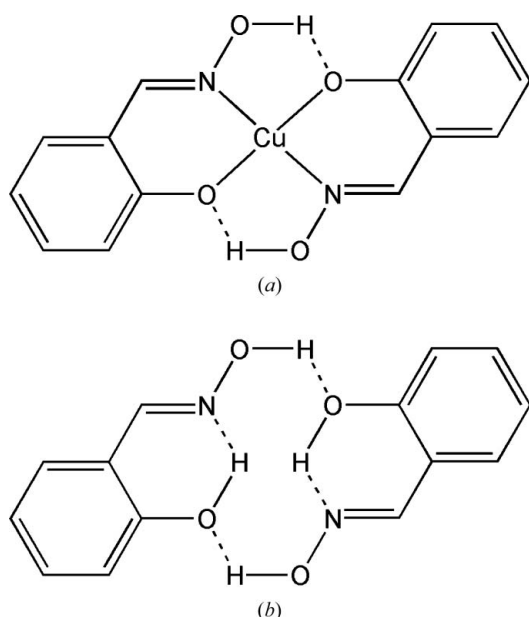


The crystal structure of the parent compound salicylaldoxime, (1), was determined using X-ray diffraction by Pfluger & Harlow (1973) [Cambridge Structural Database (CSD, Version 5.27; Allen, 2002) refcode SALOXM]. We refer to the phase investigated by these workers as salicylaldoxime-I. We have recently shown that salicylaldoxime-I undergoes a phase transition at 5.3 GPa to a second phase, salicylaldoxime-II (Wood *et al.*, 2006).

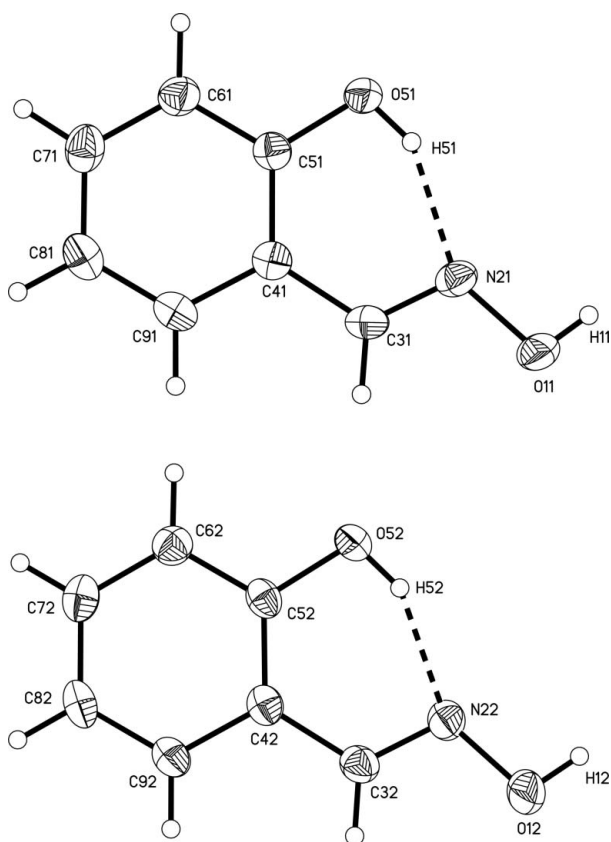
Salicylaldoxime-I crystallizes in space group  $P2_1/n$ . Pairs of molecules, related by inversion centres, form intermolecular  $\text{O}-\text{H}\cdots\text{O}$  hydrogen bonds to produce a dimer (Fig. 1*b*), for which the graph-set descriptor is  $R_4^4(10)$  (Bernstein *et al.*, 1995). This dimeric form closely resembles the pseudo-macrocylic arrangement observed in metal complexes, and is only observed in the free ligands in the solid state in salicylaldoxime derivatives which carry small substituents [*e.g.* CSD

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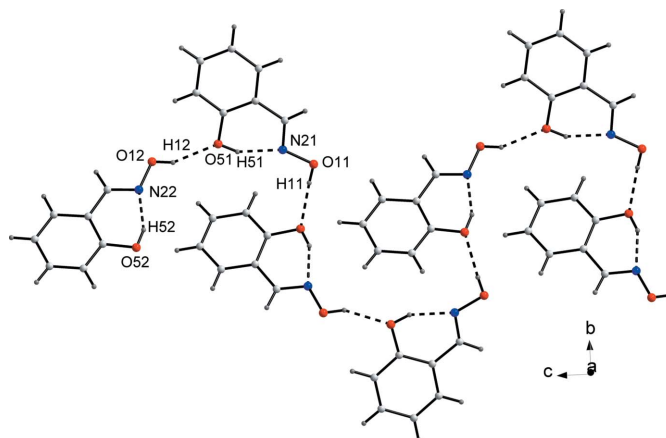
Accepted 15 August 2006

**Figure 1**

Pseudomacrocycle formation by salicylaldoxime. (a) Salicylaldoxime complexation by copper(II). (b) Hydrogen-bonded dimers formed in the crystal structure of salicylaldoxime-I. Dashed lines indicate hydrogen bonds.

**Figure 2**

The two molecules comprising the asymmetric unit of salicylaldoxime-III. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as circles of arbitrary radii. Dashed lines indicate hydrogen bonds.

**Figure 3**

Hydrogen-bonded chains in salicylaldoxime-III. Dashed lines indicate hydrogen bonds.

refcodes ABULIT (Xu *et al.*, 2004) and CLSALX (Simonsen *et al.*, 1961)]. Bulky alkyl substituents lead to hydrogen-bonded chain motifs in preference to rings [e.g. CSD refcodes HEPKET10 (Kozioł & Kosturkiewicz, 1984) and HELBOP (Maurin, 1994)].

We now report the crystal structure of a third polymorph of salicylaldoxime, salicylaldoxime-III, obtained under ambient conditions by recrystallization from a solution of hexane and chloroform. Weissenberg photographs, taken using a crystal of salicylaldoxime obtained from alcohol, were indexed by Merritt & Schroeder (1956) on the basis of an orthorhombic cell with dimensions  $a = 12.69$ ,  $b = 13.51$  and  $c = 7.98$  Å, although no coordinates were determined. These cell dimensions closely resemble those determined here for salicylaldoxime-III. In the same paper, the authors report a powder pattern, which Pfluger & Harlow (1973) claim actually corresponds to the monoclinic form, salicylaldoxime-I. However, a powder pattern simulated (using *PLATON*; Spek, 2006) on the basis of the structural parameters reported here for phase III more closely resembles the data reported by Merritt & Schroeder (1956) than the pattern calculated for phase I (sourcing coordinates from CSD refcode SALOXM). For example, the first six simulated  $d$  spacings for form III are 6.89, 6.36, 5.89, 5.74, 5.04 and 4.61 Å; the corresponding data for phase I are 9.59, 6.54, 6.26, 4.82, 4.71 and 4.50 Å, while the data reported by Merritt & Schroeder are 6.76, 6.32, 5.99, 5.68, 5.10 and 4.58 Å. We therefore disagree with Pfluger & Harlow's conclusion regarding the pattern reported by Merritt & Schroeder.

Salicylaldoxime-III is characterized by the formation of hydrogen-bonded chains rather than hydrogen-bonded rings. There are two molecules in the asymmetric unit of salicylaldoxime-III (Fig. 2), which alternate along a hydrogen-bonded chain formed by intermolecular oximic O—H $\cdots$ O hydrogen bonds (Fig. 3). The chains run along the crystallographic  $c$  axis, being generated by a  $\cdot 2_1$  operation. Intramolecular phenolic O—H $\cdots$ N hydrogen bonds are also formed (Fig. 3).

The chains interact with each other *via*  $\pi$ – $\pi$  stacking contacts formed between two symmetry-independent molecules. Within these stacking interactions, the atoms forming the phenyl ring of molecule 2 (based on O12 *etc.*) lie between 3.394 (2) and 3.519 (2) Å from the mean plane of molecule 1 (based on O11). The dihedral angle between the two phenyl planes is 2.69 (5)°.

## Experimental

Salicylaldoxime was obtained from Acros. The solid was dissolved in chloroform and enough hexane was added to induce precipitation of a small quality of solid. Chloroform was added to redissolve the precipitated solid, and the solution was filtered into a small beaker through glass wool. Crystals of salicylaldoxime grew on allowing the solution to evaporate over the course of 5 d at room temperature.

### Crystal data

$C_7H_7NO_2$	$Z = 8$
$M_r = 137.14$	$D_x = 1.398 \text{ Mg m}^{-3}$
Orthorhombic, $P2_12_12_1$	Mo $K\alpha$ radiation
$a = 7.6691$ (2) Å	$\mu = 0.10 \text{ mm}^{-1}$
$b = 12.7162$ (3) Å	$T = 150 \text{ K}$
$c = 13.3652$ (3) Å	Block, colourless
$V = 1303.40$ (5) Å <sup>3</sup>	$0.42 \times 0.25 \times 0.18 \text{ mm}$

### Data collection

Bruker SMART APEX CCD area-detector diffractometer	15665 measured reflections
$\omega$ scans	1886 independent reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 2006)	1618 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.740$ , $T_{\max} = 0.980$	$R_{\text{int}} = 0.061$
	$\theta_{\max} = 28.9^\circ$

### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F^2) + (0.04P)^2]$ , where $P = [\max(F_o^2, 0) + 2F_c^2]/3$
$R[F^2 > 2\sigma(F^2)] = 0.033$	$(\Delta/\sigma)_{\max} < 0.001$
$wR(F^2) = 0.079$	$\Delta\rho_{\max} = 0.22 \text{ e Å}^{-3}$
$S = 0.94$	$\Delta\rho_{\min} = -0.28 \text{ e Å}^{-3}$
1886 reflections	Extinction correction: Larson
194 parameters	(1970), equation 22
H atoms treated by a mixture of independent and constrained refinement	Extinction coefficient: $2.2(2) \times 10^2$

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
O11–H11 $\cdots$ O52 <sup>i</sup>	0.81 (2)	2.01 (2)	2.8137 (17)	176 (2)
O12–H12 $\cdots$ O51 <sup>ii</sup>	0.87 (2)	1.99 (2)	2.7945 (18)	155 (2)
O51–H51 $\cdots$ N21	0.86 (2)	1.85 (2)	2.6384 (18)	152 (2)
O52–H52 $\cdots$ N22	0.85 (2)	1.84 (2)	2.6285 (18)	153.4 (19)

Symmetry codes: (i)  $-x + 1, y + \frac{1}{2}, -z + \frac{1}{2}$ ; (ii)  $x + \frac{1}{2}, -y + \frac{1}{2}, -z + 1$ .

H atoms on O atoms (H11, H51, H12 and H52) were found in a difference Fourier map and their positions refined, subject to O–H distance restraints of 0.84 (5) Å and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{O})$ . The remaining H atoms were positioned geometrically and constrained to ride on their host atoms, with C–H = 0.93–0.96 Å and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ .

Data on this light-atom structure were collected with Mo  $K\alpha$  radiation, and dispersion effects are negligible. The absolute configuration of the crystal used for data collection has not been determined in this study. Friedel pairs were merged.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT; data reduction: SAINT (Bruker, 2003); program(s) used to solve structure: SIR92 (Altomare *et al.*, 1994); program(s) used to refine structure: CRYSTALS (Betteridge *et al.*, 2003); molecular graphics: DIAMOND (Brandenburg, 2006) and XP (Sheldrick, 1997); software used to prepare material for publication: CRYSTALS and PLATON (Spek, 2006).

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